



SEQUENCE LISTING

<110> LEUNG, Shui-on  
HANSEN, Hans

<120> IMMUNOCONJUGATES AND HUMANIZED ANTIBODIES SPECIFIC FOR B-CELL  
LYMPHOMA AND LEUKEMIA CELLS

<130> 18733/0996

<140> US 09/741,843

<141> 2000-12-22

<150> US 09/127,902

<151> 1998-08-03

<150> US 08/690,102

<151> 1996-07-31

<150> US 08/289,576

<151> 1994-08-12

<160> 25

<170> PatentIn version 3.1

<210> 1

<211> 339

<212> DNA

<213> Murinae gen. sp.

<220>

<221> CDS

<222> (1)..(339)

<223>

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gaa aac gtc act atg agc tgt aag tcc agt caa agt gtt tta tac agt	96
Glu Asn Val Thr Met Ser Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser	
20 25 30	

gca aat cac aag aac tac ttg gcc tgg tac cag cag aaa cca ggg cag	144
Ala Asn His Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln	
35 40 45	

tct cct aaa ctg ctg atc tac tgg gca tcc act agg gaa tct ggt gtc	192
Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val	
50 55 60	

cct gat cgc ttc aca ggc agc gga tct ggg aca gat ttt act ctt acc	240
Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr	
65 70 75 80	

atc agc aga gta caa gtt gaa gac ctg gca att tat tat tgt cac caa	288
Ile Ser Arg Val Gln Val Glu Asp Leu Ala Ile Tyr Tyr Cys His Gln	
85 90 95	

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tac ctc tcc tcg tgg acg ttc ggt gga ggg acc aag ctg gag atc aaa 336  
 Tyr Leu Ser Ser Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys  
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cgt 339  
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<210> 2  
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                   20                  25                  30

Ala Asn His Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln  
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Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val  
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Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr  
 65                  70                  75                  80

Ile Ser Arg Val Gln Val Glu Asp Leu Ala Ile Tyr Tyr Cys His Gln  
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 tca gtg aag atg tcc tgc aag gct tct ggc tac acc ttt act agc tac 96  
 Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr  
 20 25 30  
 tgg ctg cac tgg ata aaa cag agg cct gga cag ggt ctg gaa tgg att 144  
 Trp Leu His Trp Ile Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile  
 35 40 45  
 gga tac att aat cct agg aat gat tat act gag tac aat cag aac ttc 192  
 Gly Tyr Ile Asn Pro Arg Asn Asp Tyr Thr Glu Tyr Asn Gln Asn Phe  
 50 55 60  
 aag gac aag gcc aca ttg act gca gac aaa tcc tcc agc aca gcc tac 240  
 Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr  
 65 70 75 80  
 atg caa ctg agc agc ctg aca tct gag gac tct gca gtc tat tac tgt 288  
 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys  
 85 90 95  
 gca aga agg gat att act acg ttc tac tgg ggc caa ggc acc act ctc 336  
 Ala Arg Arg Asp Ile Thr Thr Phe Tyr Trp Gly Gln Gly Thr Thr Leu  
 100 105 110  
 aca gtc tcc tcg 348  
 Thr Val Ser Ser  
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<400> 4  
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 Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr  
 20 25 30  
 Trp Leu His Trp Ile Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile  
 35 40 45  
 Gly Tyr Ile Asn Pro Arg Asn Asp Tyr Thr Glu Tyr Asn Gln Asn Phe  
 50 55 60

Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr  
65 70 75 80

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys  
85 90 95

Ala Arg Arg Asp Ile Thr Thr Phe Tyr Trp Gly Gln Gly Thr Thr Leu  
100 105 110

Thr Val Ser Ser  
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<212> DNA  
<213> Homo sapiens

<220>  
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gat agg gtc act atg agc tgt aag tcc agt caa agt gtt tta tac agt 96  
Asp Arg Val Thr Met Ser Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser  
20 25 30  
gca aat cac aag aac tac ttg gcc tgg tac cag cag aaa cca ggg aaa 144  
Ala Asn His Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys  
35 40 45  
gca cct aaa ctg ctg atc tac tgg gca tcc act agg gaa tct ggt gtc 192  
Ala Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val  
50 55 60  
cct tcg cga ttc tct ggc agc gga tct ggg aca gat ttt act ttc acc 240  
Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr  
65 70 75 80  
atc agc tct ctt caa cca gaa gac att gca aca tat tat tgt cac caa 288  
Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys His Gln  
85 90 95  
tac ctc tcc tcg tgg acg ttc ggt gga ggg acc aag gtg cag atc aaa 336  
Tyr Leu Ser Ser Trp Thr Phe Gly Gly Gly Thr Lys Val Gln Ile Lys  
100 105 110  
cgt 339  
Arg

<210> 6  
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 <212> PRT  
 <213> Homo sapiens

<400> 6

Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly  
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Asp Arg Val Thr Met Ser Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser  
 20 25 30

Ala Asn His Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys  
 35 40 45

Ala Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val  
 50 55 60

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr  
 65 70 75 80

Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys His Gln  
 85 90 95

Tyr Leu Ser Ser Trp Thr Phe Gly Gly Gly Thr Lys Val Gln Ile Lys  
 100 105 110

Arg

<210> 7  
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<220>  
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 <222> (1)..(348)  
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tca gtg aag gtc tcc tgc aag gct tct ggc tac acc ttt act agc tac 96  
 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr  
 20 25 30

tgg ctg cac tgg gtc agg cag gca cct gga cag ggt ctg gaa tgg att 144  
 Trp Leu His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile  
 35 40 45

gga tac att aat cct agg aat gat tat act gag tac aat cag aac ttc 192  
 Gly Tyr Ile Asn Pro Arg Asn Asp Tyr Thr Glu Tyr Asn Gln Asn Phe  
 50 55 60

aag gac aag gcc aca ata act gca gac gaa tcc acc aat aca gcc tac 240  
 Lys Asp Lys Ala Thr Ile Thr Ala Asp Glu Ser Thr Asn Thr Ala Tyr  
 65 70 75 80

atg gag ctg agc agc ctg agg tct gag gac acg gca ttt tat ttt tgt 288  
 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Phe Tyr Phe Cys  
 85 90 95

gca aga agg gat att act acg ttc tac tgg ggc caa ggc acc acg gtc 336  
 Ala Arg Arg Asp Ile Thr Thr Phe Tyr Trp Gly Gln Gly Thr Thr Val  
 100 105 110

acc gtc tcc tcg 348  
 Thr Val Ser Ser  
 115

<210> 8  
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 <212> PRT  
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 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr  
 20 25 30

Trp Leu His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile  
 35 40 45

Gly Tyr Ile Asn Pro Arg Asn Asp Tyr Thr Glu Tyr Asn Gln Asn Phe  
 50 55 60

Lys Asp Lys Ala Thr Ile Thr Ala Asp Glu Ser Thr Asn Thr Ala Tyr  
 65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Phe Tyr Phe Cys  
 85 90 95

Ala Arg Arg Asp Ile Thr Thr Phe Tyr Trp Gly Gln Gly Thr Thr Val  
 100 105 110

Thr Val Ser Ser  
 115

<210> 9  
 <211> 116  
 <212> PRT  
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<400> 9

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 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr  
 20 25 30

Trp Leu His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile  
 35 40 45

Gly Tyr Ile Asn Pro Arg Asn Asp Tyr Thr Glu Tyr Asn Gln Asn Phe  
 50 55 60

Lys Asp Lys Ala Thr Ile Thr Ala Asp Glu Ser Thr Asn Thr Ala Tyr  
 65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Phe Tyr Phe Cys  
 85 90 95

Ala Arg Arg Asp Ile Thr Thr Phe Tyr Trp Gly Gln Gly Thr Thr Val  
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Thr Val Ser Ser  
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 ctgatgaccc aggtttcttg acttcagcc 149

<210> 11  
<211> 134  
<212> DNA  
<213> Artificial Sequence

<220>  
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ctgctcagct ccatgtaggc tgtattgggtg gattcgtctg cagttattgt ggccttgtec 120  
ttgaagttct gatt 134

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<212> DNA  
<213> Unknown

<220>  
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<210> 13  
<211> 33  
<212> DNA  
<213> Unknown

<220>  
<223> Primer

<400> 13  
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<210> 14  
<211> 49  
<212> DNA  
<213> Unknown

<220>  
<223> Primer

<400> 14  
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<210> 15  
<211> 44  
<212> DNA  
<213> Unknown

<220>  
<223> Primer

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<210> 16  
 <211> 150  
 <212> DNA  
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 <220>  
 <223> Synthetic sequence  
  
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 agtgacccta tctccaacag atgcgctcag 150  
  
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 <212> DNA  
 <213> Unknown  
  
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 <223> Primer  
  
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 <220>  
 <223> Synthetic sequence  
  
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 <212> DNA  
 <213> Unknown

<220>  
 <223> Primer

<400> 20  
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<210> 21  
 <211> 33  
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 <213> Unknown

<220>  
 <223> Primer

<400> 21  
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<210> 22  
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 <213> Murinae gen. sp.

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 agatccgctg cctgtgaagc gatcagggac accagattcc ctagtggatg cccagtagat 180  
 cagcagttta ggagactgcc ctggtttctg ctggtaccag gccaagtagt tcttgtgatt 240  
 tgcactgtat aaaacacttt gactggactt acagctcata gtgacgtttt ctctgcaga 300  
 cacagccaga gatgatggag actgggtcag ctgaatgtc 339

<210> 23  
 <211> 348  
 <212> DNA  
 <213> Murinae gen. sp.

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 ggaggatttg tctgcagtca atgtggcctt gtccttgaag ttctgattgt actcagtata 180  
 atcattccta ggattaatgt atccaatcca ttccagaccc tgtccaggcc tctgttttat 240  
 ccagtgcagc cagtagctag taaaggtgta gccagaagcc ttgcaggaca tcttcactga 300  
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<210> 24  
 <211> 339  
 <212> DNA  
 <213> Homo sapiens

<400> 24  
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 agatccgctg ccagagaatc gcgaagggac accagattcc ctagtggatg cccagtagat 180  
 cagcagttta ggtgctttcc ctggtttctg ctggtaccag gccaagtagt tcttgtgatt 240  
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 tgcgctcaga gatgatggag actggggtcag ctgaatgtc 339

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 <213> Homo sapiens

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 ggtggattcg tctgcagtta ttgtggcctt gtccttgaag ttctgattgt actcagtata 180  
 atcattccta ggattaatgt atccaatcca ttccagaccc tgtccagggtg cctgcctgac 240  
 ccagtgcagc cagtagctag taaaggtgta gccagaagcc ttgcaggaga ccttcactga 300  
 tgacccaggt ttcttgactt cagccctga ttggaccagc tggacctg 348